



STIC Search Report

Biotech-Chem Library

File Copy
09/747,385
updated

STIC Database Tracking Number: 141924

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Thursday, January 06, 2005

Case Serial Number: 09/747385

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David
Sent: Wednesday, January 05, 2005 9:15 AM
To: O'Bryen, Barbara; Fredman, Jeffrey
Subject: RE: problem re: us09747385

Yes, I apologize for not indicating that...please cancel the oligomer search portion. In retrospect, it appears I should not have included it in the first place.

Dave.

-----Original Message-----

From: O'Bryen, Barbara
Sent: Wednesday, January 05, 2005 9:14 AM
To: Fredman, Jeffrey
Cc: Lambertson, David
Subject: FW: problem re: us09747385

Jeff,
I'll let you know the new processing times when I set up the search. What you've recommended will definitely reduce the processing time. I have one question - has the oligmer portion of the search request been cancelled, or should I also do an oligomer search on the selected fragments.
Thanks,
Barb

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 8:42 AM
To: O'Bryen, Barbara
Subject: FW: problem re: us09747385

Barb,

Here is what Jeff recommended as far as improving the search. Let me know if there is anything else you need from me.

THanks a bunch,
Dave.

-----Original Message-----

From: Fredman, Jeffrey
Sent: Wednesday, January 05, 2005 7:58 AM
To: Lambertson, David
Subject: RE: problem re: us09747385

David,

I looked at the case and it is clear that for SEQ ID NOs: 6 and 15, you really only need to search a small part to see if they are out there. Since the claims are comprising and no fragments are claimed, a perfect match is essentially required. So a search of each end of the DNAs would tell you if there are any perfect hits. If there are any, it is very easy for stic to align one or two hits with the sequence at issue.

So I would recommend search nucleotides 1-250 and 9700-9955 of SEQ ID NO: 15 only. For SEQ ID NO: 6, search nucleotides 1-250 and nucleotides 5600-5887 or so. This search will run somewhat faster (If Barb could let me know how much, I would really appreciate it).

Jeff Fredman

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 6:57 AM
To: Fredman, Jeffrey

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2591.45 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatcttaatttttaatt 288

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92.6	32.2	1119	9	AG376945 Mus muscu
2	91.8	31.9	889	9	CNS006W4 Drosophil
3	91.4	31.7	951	8	AZ676519 Drosophil
4	89	30.9	889	9	CNS006W4 Drosophil
5	88.4	30.7	417	9	CNS02AH7 Drosophil
6	88.4	30.7	1221	9	AG360812 Tetraodon
7	88.2	30.6	951	8	AZ676519 Drosophil
8	87.4	30.3	613	8	AQ922590 RPTC-23-2
9	86.8	30.1	1119	9	AG376945 Mus muscu
10	86.4	30.0	613	8	AQ922590 RPTC-23-2
11	85.8	29.8	417	9	AG376945 Mus muscu
12	85.2	29.7	939	8	BH163549 Tetraodon
13	85.2	29.6	433	9	CNS04FGC Tetraodon
14	85.2	29.6	1101	9	CNS00LT2 Tetraodon
15	84.6	29.4	1295	9	CG757539 Drosophil
16	84.2	29.2	1263	9	AG376945 Mus muscu
17	84	29.2	868	8	AZ676519 Drosophil
18	83.8	29.1	875	9	CL142825 ISB1-120N
19	83.2	28.9	875	9	CL142825 ISB1-120N
20	83.2	28.9	1275	9	CL033318 CH216-36F
21	82.8	28.7	706	7	CF872119 trico29xp
22	82.6	28.7	939	8	BH163549 Tetraodon
23	82.6	28.7	997	6	CD049644 AGENCOURT
24	82.4	28.6	433	9	CNS04FGC Tetraodon

C 25 82.4 28.6 868 8 AZ673655
C 26 82 28.5 777 9 CNS025WB Tetraodon
C 27 82 28.5 1152 9 CL499024 SAILU_662
C 28 81.8 28.4 1191 9 AG360928 Mus muscu
C 29 81.8 28.4 1616 3 CR734259 Tetraodon
C 30 81.4 28.3 1101 9 CNS0021J Drosophil
C 31 81.4 28.3 1190 9 CNS02ON7 Tetraodon
C 32 80.8 28.1 1014 6 CD048535 AGENCOURT
C 33 80.6 28.0 1201 9 CNS0167M Drosophil
C 34 80.2 27.8 483 9 CNS0119C Drosophil
C 35 80.2 27.8 741 7 CN842216 AGENCOURT
C 36 79.8 27.7 908 8 BH156237 ENTRV74TF
C 37 79.8 27.7 1225 9 AG360812 Mus muscu
C 38 79.6 27.6 1221 9 AG360812 Mus muscu
C 39 79.4 27.6 866 9 CNS006MS AGENCOURT
C 40 79.4 27.6 1067 6 CD386564 AGENCOURT
C 41 79.2 27.5 706 7 CF872119 trico29xp
C 42 78.8 27.4 437 9 CNS03OF0 Tetraodon
C 43 78.8 27.4 866 6 CF289423 AGENCOURT
C 44 78.8 27.4 922 8 AZ548363 AGENCOURT
C 45 78.4 27.2 641 1 AV735039 AV735039

ALIGNMENTS

RESULT 1
LOCUS AG376945
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-184M01.T7, genomic survey sequence.
ACCESSION AG376945
VERSION AG376945.1 GI:47988150
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1119)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsukuba, Ibaraki, 305-0874 Japan
COMMENT (E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@tc.riken.jp).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
e-mail: abe@tc.riken.jp
phone: 81-298-36-9189, fax: 81-298-36-9199
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 1119
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-184M01.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

COMMENT

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1314.48 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887
Perfect score: 288
Sequence: 1 agtcaatcaaaaaataaa.....atcatctaaattttaaaatt 288

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	76.2	26.5	3673778	15	US-10-312-841-2
C 2	75.8	26.3	10039	15	Sequence 2, Appli
C 3	72.6	25.2	585	18	Sequence 2015, Ap
C 4	69.8	24.2	5908	14	Sequence 58104, A
C 5	69.8	24.2	5908	15	Sequence 93, Appl
C 6	69.8	24.2	5908	15	Sequence 105, App
C 7	69.6	24.2	6486	17	Sequence 175, App
C 8	68.6	23.8	529	18	Sequence 80, Appl
C 9	68.6	23.8	543	17	Sequence 171364, A
C 10	68.2	23.7	433	17	Sequence 14156, A
C 11	67.8	23.5	474	18	Sequence 4250, Ap
C 12	67.8	23.5	545	16	Sequence 2807, Ap
					Sequence 142212,

13	67.6	23.5	584	18	US-10-425-115-33678	Sequence 33678, A
14	67.2	23.3	8946	15	US-10-311-455-883	Sequence 883, App
15	67.2	23.3	3673778	15	US-10-312-841-1	Sequence 1, Appli
16	67	23.3	438	16	US-10-424-599-79137	Sequence 79137, A
17	66.8	23.2	317	9	US-09-960-352-3699	Sequence 2699, Ap
18	66.6	23.1	510	18	US-10-357-930-58133	Sequence 58133, A
19	66.4	23.1	461	10	US-09-814-353-17724	Sequence 17724, A
20	66.2	23.0	423	10	US-09-918-995-7147	Sequence 7147, Ap
C 21	66	22.9	6436	15	US-10-311-455-654	Sequence 654, App
C 22	65.8	22.8	403	18	US-10-425-115-155989	Sequence 155989,
C 23	65.8	22.8	1543	16	US-10-262-839-165	Sequence 165, App
24	65.4	22.7	317	18	US-10-357-930-58200	Sequence 58200, A
25	65.4	22.7	603	18	US-10-357-930-58664	Sequence 58664, A
C 26	65.4	22.7	12138	15	US-10-311-455-1601	Sequence 1601, Ap
C 27	65.4	22.7	12138	16	US-10-257-166-115	Sequence 115, App
C 28	64.6	22.4	368	17	US-10-021-323-5024	Sequence 5024, Ap
29	64.6	22.4	545	17	US-10-021-323-6889	Sequence 6889, Ap
30	64.4	22.4	390	16	US-10-424-599-72814	Sequence 72814, A
31	64.4	22.4	565	18	US-10-425-115-48405	Sequence 48405, A
C 32	64.4	22.4	6171	15	US-10-311-455-762	Sequence 762, App
33	64.2	22.3	1403	17	US-10-437-963-19360	Sequence 19360, A
34	64.2	22.3	8056	18	US-10-473-126-240	Sequence 240, App
C 35	64	22.2	5753	17	US-10-433-793-146	Sequence 146, App
36	63.8	22.2	530	18	US-10-425-115-88475	Sequence 88475, A
37	63.6	22.1	799	16	US-10-424-599-88818	Sequence 88818, A
38	63.6	22.1	1243	18	US-10-425-115-133710	Sequence 133710,
39	63.2	21.9	452	17	US-10-021-323-4768	Sequence 4768, Ap
40	63.2	21.9	564	17	US-10-021-323-7972	Sequence 7972, Ap
41	63.2	21.9	1245	18	US-10-425-115-15266	Sequence 15266, A
C 42	63.2	21.9	6112	15	US-10-311-455-636	Sequence 636, App
C 43	63.2	21.9	21537	15	US-10-311-455-1972	Sequence 1972, Ap
C 44	63.2	21.9	3673778	15	US-10-312-841-2	Sequence 2, Appli
45	63	21.9	457	17	US-10-437-963-70141	Sequence 70141, A

ALIGNMENTS

RESULT 1
US-10-312-841-2/c
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312.841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match	26.5%	Score 76.2;	DB 15;	Length 3673778;
Best Local Similarity	54.9%	Pred. No. 0.065;		
Matches 150;	Conservative 0;	Mismatches 123;	Indels 0;	Gaps 0;
Qy	5	AATCAAAAAATATAATATAATTAATCTACTAAGAGAGTTTAATGAAAGAGAGAGC 64		
Db	971677	AA 971618		
Qy	65	TTACGATTAGAGAGAAATATAAAAGAGATGCGAGAGACTAAATAATTAATTAAGAG 124		
Db	971617	AA 971558		
Qy	125	AGGTATAGTATAATACCTCTTCTTTTAAAGTGGCTTAAATTTGATTTTAGAGCTTCA 184		

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 64.5517 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataaa.....atcatctaaatttttaatt 288

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71.2	24.7	196	US-09-442-054A-42	Sequence 42, Appl
2	71.2	24.7	196	US-09-442-054A-42	Sequence 42, Appl
3	59.6	20.7	731	US-08-451-405A-2	Sequence 2, Appl
4	58.8	20.4	5852	US-07-867-106-2	Sequence 2, Appl
5	58.4	20.3	2621	US-08-553-619B-8	Sequence 8, Appl
6	56.4	19.6	8607	US-10-204-708-72	Sequence 72, Appl
7	56.4	19.6	1684976	US-08-916-421B-1	Sequence 1, Appl
8	56.4	19.6	1684976	US-09-692-570-1	Sequence 1, Appl
9	56.2	19.5	1577	US-09-270-767-3138	Sequence 3138, Ap
10	56.2	19.5	1577	US-09-270-767-3138	Sequence 18420, A
11	55.8	19.4	20674	US-09-641-638-651	Sequence 651, App
12	55.8	19.4	20674	US-10-170-097-651	Sequence 651, App
13	55.5	19.1	6243	US-09-056-075-1	Sequence 1, Appl
14	54.6	19.0	3138	US-07-867-106-4	Sequence 4, Appl
15	54	18.8	3440	US-08-471-791-27	Sequence 27, Appl
16	54	18.8	3440	PCT-US91-01746-27	Sequence 27, Appl
17	53.6	18.6	8607	US-10-204-708-71	Sequence 71, Appl
18	52.8	18.3	5455	US-10-204-708-34	Sequence 34, Appl
19	52.6	18.3	731	US-08-451-405A-2	Sequence 3, Appl
20	52.6	18.3	2146	US-10-003-392-3	Sequence 3, Appl
21	52.6	18.3	3275	US-09-370-838-151	Sequence 151, App
22	52.6	18.3	3275	US-09-854-133-151	Sequence 151, App
23	52.4	18.2	5152	US-10-204-708-47	Sequence 47, Appl
24	52.4	18.2	6070	US-10-204-708-9	Sequence 9, Appl
25	52.4	18.2	10619	US-10-204-708-4	Sequence 4, Appl
26	52.2	18.1	1738	US-09-918-909A-27	Sequence 27, Appl
27	52.2	18.1	3138	US-07-867-106-4	Sequence 4, Appl

c	28	52.2	18.1	6113	4	US-10-204-708-14	Sequence 14, Appl
	29	52.1	18.1	396	4	US-09-640-173-10	Sequence 10, Appl
	30	52.1	18.1	396	4	US-09-713-550-10	Sequence 10, Appl
	31	52.1	18.1	396	4	US-09-825-294-10	Sequence 10, Appl
	32	52.1	18.1	396	4	US-09-970-966-10	Sequence 10, Appl
	33	52.1	18.1	3440	1	US-08-471-791-27	Sequence 27, Appl
	34	52.1	18.1	3440	5	PCT-US91-01746-27	Sequence 27, Appl
	35	52	18.1	6265	4	US-09-129-112-3	Sequence 3, Appl
c	36	51.8	18.0	4185	4	US-09-417-485D-7	Sequence 7, Appl
	37	51.8	18.0	6243	2	US-09-056-075-1	Sequence 1, Appl
	38	51.6	17.9	473	1	US-08-764-100-16	Sequence 16, Appl
	39	51.6	17.9	473	1	US-08-764-100-16	Sequence 16, Appl
	40	51.6	17.9	3198	3	US-08-842-306B-48	Sequence 48, Appl
	41	51.6	17.9	3198	3	US-08-838-973B-48	Sequence 48, Appl
	42	51.6	17.9	3199	4	US-09-945-249-10	Sequence 10, Appl
c	43	51.6	17.9	3199	4	US-09-041-990-10	Sequence 10, Appl
	44	51.6	17.9	4970	1	US-08-764-100-14	Sequence 14, Appl
	45	51.6	17.9	4970	1	US-08-764-100-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-442-054A-42
; Sequence 42, Application US/09442054A
; Patent No. 6770738
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf H.
; APPLICANT: Mollegaard, Neils E.
; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
; FILE REFERENCE: ISIS4290
; CURRENT APPLICATION NUMBER: US/09/442,054A
; PRIORITY FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 08/471,907
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/ EP92/01219
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-42

Query Match	24.7%	Score	71.2	DB	4	Length	196
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Gaps	0						
Qy	34	AAAGAAGACTTAATGAAAAAGAAAAAGAGCTTCACGAATTAGAGAAAAATATAAAAAAGA	93				
Db	1	AA	60				
Qy	94	ATGCAAGAACTAAATAATTAATAAAGAGAGGTATAGTATATACCTCTTCTTTT	153				
Db	61	AA	120				
Qy	154	TAAGTGCCTAAATGATTTTAGAGCTTCATTTTTTCACTTTCTTCTTCCT	213				
Db	121	TT	180				
Qy	214	TTTCTATATCTTTTT	229				
Db	181	TTTTTTTTTTTTTTTT	196				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 304.828 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatctaaatctttaatt 288

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001s:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84.4	29.3	435	4	AAI82079 Human pol
2	75.8	26.3	10039	6	ABL34042 Human imm
3	72.8	25.3	380	4	AAI80354 Human pol
4	72.6	25.2	585	5	ABV58085 Human pro
5	69.8	24.2	5908	4	AA545386 Chemical
6	69.8	24.2	5908	6	ABK28231 DNA trans
7	69.8	24.2	5908	6	AA561216 Human gen
8	69.6	24.2	6486	6	ABQ67050 Human ang
9	69	24.0	364	4	AAI84912 Human pol
10	68.2	23.7	433	9	ACH17038 Human pol
11	67.2	23.3	8946	6	ABL32910 Human imm
12	66.8	23.2	317	8	ABX37534 Bovine ES
13	66.6	23.1	361	4	AAI85935 Human pol
14	66.6	23.1	510	5	ABV58114 Human pro
15	66.4	23.1	461	5	ADL43834 Human ova
16	66.2	23.0	423	9	ACH19335 Human adu
17	66	22.9	6436	6	ABL32681 Human imm
18	65.8	22.8	1543	8	ACCT2157 Human NOV
19	65.8	22.8	6162	8	ABK31331 Signal tr
20	65.4	22.7	317	5	ABV58181 Human pro
21	65.4	22.7	603	5	ABV58645 Human pro

C 22	65.4	22.7	12138	6	ABK40033	Human che
C 23	65.4	22.7	12138	6	ABL33628	Human imm
C 24	64.4	22.4	6171	6	ABL32789	Human imm
C 25	64.2	22.3	8056	8	ABZ10100	Haematopo
C 26	64	22.2	5753	6	ABQ67116	Human ang
C 27	64	22.2	50000	6	ABL55644	AmEPV gen
C 28	63.2	21.9	6112	6	ABL32663	Human imm
C 29	63.2	21.9	21537	6	ABL33999	Human imm
C 30	62.8	21.8	3101	2	AAQ02047	Sequence
C 31	62.8	21.8	3744	3	AAA70149	Plasmodi
C 32	62.8	21.8	9095	6	ABQ67061	Human ang
C 33	62.6	21.7	461	9	ACH28231	Human adu
C 34	62.6	21.7	8056	8	ABZ10246	Haematopo
C 35	62.4	21.7	700	4	AAH93026	Human inf
C 36	62.4	21.7	6025	4	AA545339	Chemical
C 37	62.4	21.7	6057	6	ABL31397	Signal tr
C 38	62.4	21.7	6057	6	ABL70362	Chemical
C 39	62.2	21.6	324	4	AAI82686	Human pol
C 40	62.2	21.6	419	4	AAI89272	Human pol
C 41	62	21.5	6577	6	ABL33356	Human imm
C 42	62	21.5	6577	6	ABL70561	Chemical
C 43	62	21.5	6577	6	AA561221	Human gen
C 44	61.8	21.5	480	9	ACH25001	Human adu
C 45	61.6	21.4	461	5	ADL43834	Human ova

ALIGNMENTS

RESULT 1

AAI82079

ID AAI82079 standard; cDNA; 435 BP.

XX

AC AAI82079;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 2139.

DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation; ss.

OS Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX P-PSDB; AAO02148.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 1; SEQ ID NO 2139; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO3910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1399.17 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatctaaatctttaatt 288

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_str.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	5887	1	AF159249
2	284.8	98.9	6281	1	AF022647
3	81.2	28.2	38692	3	AC116919
4	80.2	27.8	333321	3	AC116986
5	78.8	27.4	88549	3	AC116924
6	78.4	27.2	105682	3	AC116957_3
7	77.6	26.9	110000	3	AC116957_0
8	77.4	26.9	302156	3	AC116977
9	77	26.7	156975	2	CR394534
10	76.2	26.5	110000	3	AC116984_1
11	76.2	26.5	349880	6	AX344566
12	76	26.4	2781	3	AY044085
13	75.8	26.3	10039	6	AX346944
14	75.8	26.3	125623	3	AC115599
15	75.8	26.3	266544	3	AC116956
16	75.8	26.3	273275	3	AE014828
17	75.4	26.2	105320	3	AC116920
18	75.4	26.2	178273	2	AC005308
19	75.4	26.2	250531	3	AE014845

20	75.2	26.1	192187	3	AC117072
21	74.8	26.0	156978	2	CR339045
22	74.4	25.8	132254	3	AC116330
23	73.8	25.6	7554	3	AY160096
24	73.8	25.6	125623	3	AC115599
25	73.8	25.6	182870	3	AC116960
26	73.6	25.6	88549	3	AC116924
27	73.4	25.5	253305	3	PFMAL387
28	73.2	25.4	4951	3	AY160092
29	73.2	25.4	110000	3	AC116957_0
30	73.2	25.4	250029	3	AE014838
31	73	25.3	61052	2	AC123513
32	73	25.3	136240	3	AC117070
33	72.8	25.3	4430	3	AY160097
34	72.8	25.3	40611	3	AC116987
35	72.8	25.3	105320	3	AC116920
36	72.8	25.3	110000	3	AC116305_3
37	72.8	25.3	192187	3	AC117072_3
38	72.6	25.2	585	6	CQ526237
39	72.6	25.2	4000	3	AF482963
40	72.6	25.2	133426	2	AC134521
41	72.6	25.2	349751	3	PFMAL4P3
42	72.4	25.1	1504	3	DDH4
43	72.2	25.1	182871	3	AC117176
44	72	25.0	39838	2	AC149329
45	72	25.0	110000	2	PFMAL7P1_06

ALIGNMENTS

RESULT 1	AF159249	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.	5887 bp	DNA	circular BCT 09-FEB-2000
LOCUS	AF159249	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.			
DEFINITION	AF159249	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.			
ACCESSION	AF159249	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.			
VERSION	AF159249.1	GI:6941824				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
C 1	81.2	32.5	544	5	BQ398892	NISC_mol2
C 2	77	30.8	843	5	CNS0091L	AL053009 Drosophill
C 3	76.4	30.6	892	6	CF289361	CF289361 Drosophill
C 4	76.4	30.6	894	7	CK158244	FKGAS03947
C 5	75.6	30.2	625	9	CNS036A2	AL229763 Tetraodon
C 6	75.6	30.2	1195	5	BUI76001	BUI76001 AGESCHORT
C 7	75.2	30.1	341	9	CNS060606	AL065612 Drosophill
C 8	75.2	30.1	454	5	BX500915	BX500915 DKF2p779D
C 9	74.8	29.9	357	9	CNS028DK	AL185825 Tetraodon
C 10	74.8	29.9	625	9	CNS036A2	AL229763 Tetraodon
C 11	74.8	29.9	795	6	CF288665	CF288665 AGESCHORT
C 12	73.6	29.4	496	8	BH182183	O20_L_21-
C 13	73.6	29.4	496	9	CNS07NMZ	AL161913 T7 and of
C 14	73.2	29.3	290	6	CB045528	CB045528 NISC_gc10
C 15	73.2	29.3	316	5	BQ523462	BQ523462 NISC_n122
C 16	73.2	29.3	367	5	BQ525045	BQ525045 NISC_no08
C 17	73.2	29.3	386	6	CB044394	CB044394 NISC_gc04
C 18	73.2	29.3	403	7	CF802125	CF802125 rj57e12.y
C 19	73.2	29.3	408	5	BX471963	BX471963 DKF2p686H
C 20	73.2	29.3	501	5	BQ525537	BQ525537 NISC_no11
C 21	73.2	29.3	519	7	CK311148	CK311148 oj58e08.y
C 22	73.2	29.3	530	5	BX566754	BX566754 BX566754
C 23	73.2	29.3	683	8	AQ329791	AQ329791 rbx50045B
C 24	73.2	29.3	806	7	CF783082	CF783082 AGESCHORT

conducted by
(University of

(University of Iowa). Note: This is a *Xenopus* Gene

FEATURES source

72 TCAATTTTCTAATTCAATCGCTTTTAAATTTCTCTAAAGTCTTTTTAATTTTTTAGTA 131

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 264.607 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-6_COPY_1_250
Perfect score: 250
Sequence: 1 catataataactttttgttt.....agccataataataaaaaa 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	72.6	29.0	556	5 ABV40163	Abv40163 Human pro
C 2	72.6	29.0	556	5 ABV40063	Abv40063 Human pro
C 3	72.6	29.0	556	5 ABV42105	Abv42105 Human pro
C 4	72.6	29.0	556	5 ABV43601	Abv43601 Human pro
C 5	72.6	29.0	626	5 ABV60941	Abv60941 Human pro
C 6	72	28.8	277	8 ABX47508	Abx47508 Bovine ES
C 7	71.6	28.6	309	5 ABV44994	Abv44994 Human pro
C 8	70.2	28.1	375	5 ABV44911	Abv44911 Human pro
C 9	70.2	28.1	774	10 ADK57243	Adk57243 Plant DNA
10	68.2	27.3	9095	6 ABQ67061	Abq67061 Human ang
11	67.8	27.1	277	8 ABX47508	Abx47508 Bovine ES
12	67	26.8	310	4 AAH71505	Aah71505 Bovine ES
13	67	26.8	419	8 ABX46069	Abx46069 Bovine ES
14	66.8	26.7	1533	12 ADQ25148	Adq25148 Human sof
15	66.6	26.6	299	5 ADI72102	Adi72102 Human ova
16	66.6	26.6	299	5 ADL37251	Adl37251 Human ova
17	66.6	26.6	626	5 ABV60941	Abv60941 Human pro
C 18	66.6	26.6	2427	2 AAQ04107	Aaq04107 Human pro
19	65.8	26.3	545	4 AAH70126	Aah70126 Human cer
20	65.8	26.3	621	4 AAH71551	Aah71551 Human cer
C 21	65.6	26.2	494	5 ABV10021	Abv10021 Human pro

C 22	65.4	26.2	903	3 AAC79727	Aac79727 Human sec
C 23	65.4	26.2	3232	10 ADD18806	Add18806 Human dis
C 24	65.2	26.1	1860	4 AAF72806	Aaf72806 Secreted
25	65.2	26.1	9963	6 ABL32694	AbL32694 Human imm
26	64.8	25.9	375	8 ABX49849	Abx49849 Bovine ES
27	64.6	25.8	268	4 AAH70080	Aah70080 Human cer
28	64.6	25.8	664	5 ADI71997	Adi71997 Human ova
29	64.6	25.8	664	5 ADL37146	Adl37146 Human ova
30	64.4	25.8	241	8 ABX42739	Abx42739 Bovine ES
31	64.4	25.8	314	8 ABX47247	Abx47247 Bovine ES
C 32	64.2	25.7	403	4 AA183197	Aa183197 Human pol
33	64	25.6	414	5 ADL37389	Adl37389 Human ova
34	64	25.6	414	5 ADI72244	Adi72244 Human ova
C 35	64	25.6	579	5 ABV58690	Abv58690 Human pro
C 36	64	25.6	4236	6 ABQ92014	Abq92014 Human pol
C 37	63.8	25.5	403	12 ADL10051	Adl10051 Cat flea
38	63.8	25.5	843	5 ABV16074	Abv16074 Human pro
39	63.6	25.4	351	5 ADL43689	Adl43689 Human ova
40	63.6	25.4	393	8 ABX39417	Abx39417 Bovine ES
41	63.6	25.4	397	8 ABX48619	Abx48619 Bovine ES
42	63.6	25.4	476	5 ADL43530	Adl43530 Human ova
C 43	63.4	25.4	421	8 ABX44057	Abx44057 Bovine ES
C 44	63.2	25.3	390	5 ADL43918	Adl43918 Human ova
C 45	63.2	25.3	4824	12 ADQ22371	Adq22371 Human sof

ALIGNMENTS

RESULT 1
ABV40163/c
ID ABV40163 standard; cDNA; 556 BP.
XX
AC ABV40163;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 40154.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
DR Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 8115; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1214.56 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-6_COPY_1_250

Perfect score: 250

Sequence: 1 catataataactttttgttt.....agccataataataaaaaa 250

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	250	100.0	5887	1	AF159249	Fusobacterium nucleatum
2	223	89.2	6281	1	AF022647	Fusobacterium nucleatum
3	72.6	29.0	556	6	CQ508215	Sequence
4	72.6	29.0	556	6	CQ508315	Sequence
5	72.6	29.0	556	6	CQ510257	Sequence
6	72.6	29.0	556	6	CQ511753	Sequence
7	72.6	29.0	556	6	CQ529093	Sequence
8	71.8	28.7	227273	2	AC141526	Rattus no
9	71.6	28.6	309	6	CQ513146	Sequence
10	71.2	28.5	177560	2	CR318627	Danio rer
11	70.8	28.3	129518	2	AC149940	Strongylo
12	70.2	28.1	375	6	CQ513063	Sequence
13	69.8	27.9	202872	2	AC016160	Homo sapi
14	69.4	27.8	110000	3	AC116984	Continuation (2 of
15	69.2	27.7	1373	10	BC049731	Mus muscu
16	69.2	27.7	1930	5	BC066725	Danio rer
17	69	27.6	182871	3	AC117176	Dictyoste
18	68.8	27.5	218404	5	BX470087	Zebrafish
19	68.6	27.4	1946	5	BC077411	Xenopus 1

20	68.4	27.4	195422	2	CR450745	Danio rer
21	68.2	27.3	9095	6	AX458545	Sequence
22	67.8	27.1	2005	9	HSN803426	Homo sapi
23	67.6	27.0	195057	2	BX897664	Danio rer
24	67.4	27.0	134597	2	CR391983	Danio rer
25	67.2	26.9	88549	3	AC116924	Dictyoste
26	67.2	26.9	343050	3	PFA929353	Plasmodiu
27	67	26.8	310	6	AX187085	Sequence
28	67	26.8	57203	3	AC115581	Dictyoste
29	66.8	26.7	90373	3	AC115680	Dictyoste
30	66.8	26.7	146570	3	AC117076	Dictyoste
31	66.8	26.7	180665	2	CR382366	Danio rer
32	66.8	26.7	349980	6	AX344559	Sequence
33	66.6	26.6	299	6	CQ397773	Sequence
34	66.6	26.6	299	6	CQ404070	Sequence
35	66.6	26.6	626	6	CQ529093	Sequence
36	66.6	26.6	192525	2	BX936428	Danio rer
37	66.6	26.6	192955	2	AC148921	Callithri
38	66.2	26.5	2725	5	BC077764	Xenopus 1
39	66.2	26.5	194883	2	CR450839	Danio rer
40	66.2	26.5	211748	2	CR392346	Danio rer
41	66	26.4	1606	10	BC051176	Mus muscu
42	66	26.4	57538	3	AC115682	Dictyoste
43	66	26.4	90373	3	AC115680	Dictyoste
44	65.8	26.3	545	6	AX185705	Sequence
45	65.8	26.3	621	6	AX187131	Sequence

ALIGNMENTS

RESULT 1	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.	5887 bp	DNA	circular BCT 09-FEB-2000
LOCUS	AF159249	AF159249.1	GI:6941824		
DEFINITION	Fusobacterium nucleatum				
ACCESSION	AF159249				
VERSION	AF159249.1				
KEYWORDS	Fusobacterium nucleatum				
SOURCE	Fusobacterium nucleatum				
ORGANISM	Fusobacterium nucleatum				
REFERENCE	1	(bases 1 to 5887)			
AUTHORS	Kinder Haake, S. and Finegold, S.M.				
TITLE	DNA sequence analysis of the Fusobacterium nucleatum plasmid, pFN1				
JOURNAL	J. Dent. Res. 78, 420 (1999)				
REFERENCE	2	(bases 1 to 5887)			
AUTHORS	Kinder Haake, S. and Yoder, S.				
TITLE	Transformation of Fusobacterium nucleatum by electroporation				
JOURNAL	Abstr. Gen. Meet. Am. Soc. Microbiol. 99, 331 (1999)				
REFERENCE	3	(bases 1 to 5887)			
AUTHORS	Haake, S.K., Yoder, S.C., Attarian, G. and Podkaminer, K.				
TITLE	Native plasmids of Fusobacterium nucleatum: characterization and use in development of genetic systems				
JOURNAL	J. Bacteriol. 182 (4), 1176-1180 (2000)				
REFERENCE	20115567				
PUBMED	10648549				
REFERENCE	4	(bases 1 to 5887)			
AUTHORS	Kinder Haake, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUN-1999) Periodontics, UCLA School of Dentistry, 10833 LeConte Avenue, Los Angeles, CA 90095-1668, USA				
FEATURES	Location/Qualifiers				
source	1. 5887				
	/organism="Fusobacterium nucleatum"				
	/mol_type="genomic DNA"				
	/strain="12230"				
	/db_xref="taxon:851"				
	/plasmid="pFN1"				
	/notes="lower-respiratory tract clinical isolate from the Wadsworth Anaerobe Laboratory, West Los Angeles Veterans Affairs Medical Center"				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2249.52 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 cacctgacgcgcctgtagc.....ggttcacgtaggggccatc 250

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	250	100.0	500	6	CD451062	CD451062 USDA-FP 1
C 2	250	100.0	528	9	CG808215	CG808215 1118090D0
C 3	250	100.0	539	9	CG801749	CG801749 1118024B0
C 4	250	100.0	581	1	AV403804	AV403804 AV403804
C 5	250	100.0	584	1	AV404063	AV404063 AV404063
C 6	250	100.0	608	1	AJ611113	AJ611113 AJ611113
C 7	250	100.0	613	1	AU250522	AU250522 AU250522
C 8	250	100.0	614	5	BQ823788	BQ823788 1030112G0
C 9	250	100.0	625	5	BQ813491	BQ813491 1030036H0
C 10	250	100.0	627	1	AV403998	AV403998 AV403998
C 11	250	100.0	627	1	AV404060	AV404060 AV404060
C 12	250	100.0	627	1	AV404091	AV404091 AV404091
C 13	250	100.0	627	1	AV404095	AV404095 AV404095
C 14	250	100.0	628	1	AV403779	AV403779 AV403779
C 15	250	100.0	628	1	AV403828	AV403828 AV403828
C 16	250	100.0	628	1	AV403918	AV403918 AV403918
C 17	250	100.0	628	1	AV403919	AV403919 AV403919
C 18	250	100.0	628	1	AV403945	AV403945 AV403945
C 19	250	100.0	628	1	AV403970	AV403970 AV403970
C 20	250	100.0	628	1	AV403997	AV403997 AV403997
C 21	250	100.0	628	1	AV404068	AV404068 AV404068
C 22	250	100.0	629	1	AV404061	AV404061 AV404061
C 23	250	100.0	630	5	BQ819966	BQ819966 1030081D0
C 24	250	100.0	642	7	CN582805	CN582805 USDA-FP_1

C 25	250	100.0	659	1	AU251092	AU251092 AU251092
C 26	250	100.0	660	1	AU248437	AU248437 AU248437
C 27	250	100.0	660	5	BQ814002	BQ814002 1030040D0
C 28	250	100.0	661	1	AU249975	AU249975 AU249975
C 29	250	100.0	663	7	CO641266	CO641266 USDA-FP 1
C 30	250	100.0	665	1	AU247386	AU247386 AU247386
C 31	250	100.0	666	6	CB550392	CB550392 MMPL0002
C 32	250	100.0	667	6	CB550481	CB550481 MMPL0002
C 33	250	100.0	676	6	CB549779	CB549779 MMPL0018
C 34	250	100.0	681	1	AV403811	AV403811 AV403811
C 35	250	100.0	681	1	AV403921	AV403921 AV403921
C 36	250	100.0	681	6	CB548636	CB548636 MMPL0018
C 37	250	100.0	683	6	CB550005	CB550005 MMPL0006
C 38	250	100.0	684	1	AV404405	AV404405 AV404405
C 39	250	100.0	685	5	BU724260	BU724260 SJMBFC05
C 40	250	100.0	689	1	AU249799	AU249799 AU249799
C 41	250	100.0	689	5	BQ819196	BQ819196 1030076B0
C 42	250	100.0	690	1	AU246979	AU246979 AU246979
C 43	250	100.0	690	1	AV405131	AV405131 AV405131
C 44	250	100.0	695	6	CB550355	CB550355 MMPL0003
C 45	250	100.0	696	6	CB549815	CB549815 MMPL0011

ALIGNMENTS

RESULT 1
CD451062/c
LOCUS CD451062 500 bp mRNA linear EST 03-JUN-2003
DEFINITION USDA-FP 103109 Adult Alate Brown Citrus Aphid Toxoptera citricida
cDNA clone WHWC-41_F12 5', mRNA sequence.
ACCESSION CD451062
VERSION CD451062.1 GI:31365802
KEYWORDS EST.
SOURCE Toxoptera citricida (brown citrus aphid)
ORGANISM Toxoptera citricida
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Toxoptera.
REFERENCE 1 (bases 1 to 500)
HUNTER, W.B., DANG, P.M., BAUSHER, M.G., CHAPARRO, J.X., MCKENDREE, W.,
SHATTERS, R.G. JR., MCKENZIE, C.L. and SINISTERA, X.H.
Aphid biology: Expressed genes from alate Toxoptera citricida, the
brown citrus aphid
J. Insect Sci. 3 (23), 1-7 (2003)
COMMENT Contact: Wayne B. Hunter
US Horticultural Research Laboratory
USDA - ARS
2001 South Rock Rd., Fort Pierce, FL 34945, USA
Tel: (772) 462-5898
Fax: (772) 462-5986
Email: whunter@ushrl.ars.usda.gov
Seq primer: T3 Primer.
Location/Qualifiers
1. 500
/organism="Toxoptera citricida"
/mol_type="mRNA"
/db_xref="taxon:223852"
/clone="WHWC-41_F12"
/sex="Mixed population"
/tissue_type="Entire insect"
/dev_stage="Adult Alate"
/lab_host="XLI-Blue"
/clone_lib="Adult Alate Brown Citrus Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Toxoptera citricida (Kirkaldy); A high quality EST
with at least 100 contiguous bases at Trace Tuner score of
20 or better."

FEATURES
source
Query Match 100.0%; Score 250; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.5e-62;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1141.04 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccctgacgcgccttagc.....gggtcagtagtgggcatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	3327	17	US-10-796-486-56
2	250	100.0	3369	17	US-10-796-486-48
3	250	100.0	3379	15	US-10-222-026A-19
4	250	100.0	3417	17	US-10-466-959-1
5	250	100.0	3417	18	US-10-466-960A-1
6	250	100.0	3450	15	US-10-222-026A-20
7	250	100.0	3497	16	US-10-420-529-11
8	250	100.0	3501	17	US-10-466-959-2
9	250	100.0	3501	18	US-10-466-960A-2
10	250	100.0	3621	18	US-10-471-607-11
11	250	100.0	3954	17	US-10-796-486-53
12	250	100.0	3954	17	US-10-796-486-57

13	250	100.0	3976	17	US-10-796-486-49
14	250	100.0	3988	15	US-10-393-269-12
15	250	100.0	4151	17	US-10-421-285-15
16	250	100.0	4188	17	US-10-466-959-3
17	250	100.0	4188	18	US-10-466-960A-3
18	250	100.0	4390	9	US-09-968-355-18
19	250	100.0	4412	18	US-10-677-777-3
20	250	100.0	4438	9	US-09-968-355-21
21	250	100.0	4516	9	US-09-968-355-24
22	250	100.0	4594	9	US-09-968-355-15
23	250	100.0	4665	9	US-09-759-960-7
24	250	100.0	4665	18	US-10-603-062-7
25	250	100.0	4677	15	US-10-237-146-7
26	250	100.0	4692	15	US-10-161-403-29
27	250	100.0	4727	15	US-10-433-640-16
28	250	100.0	4733	10	US-10-115-987B-12
29	250	100.0	4733	10	US-09-797-496B-1
30	250	100.0	4740	15	US-10-177-390-1
31	250	100.0	4740	15	US-10-115-987B-13
32	250	100.0	4748	10	US-09-796-575-4
33	250	100.0	4748	17	US-10-652-814-4
34	250	100.0	4778	15	US-10-138-998A-1
35	250	100.0	4782	15	US-10-138-998A-2
36	250	100.0	4793	18	US-10-737-290-141
37	250	100.0	4862	15	US-10-161-403-87
38	250	100.0	4883	14	US-10-006-593-111
39	250	100.0	4883	15	US-10-307-724-111
40	250	100.0	4883	18	US-10-737-290-111
41	250	100.0	4886	14	US-10-128-853-4
42	250	100.0	4894	14	US-10-055-794-2
43	250	100.0	4943	13	US-10-001-189-54
44	250	100.0	4944	13	US-10-001-189-55
45	250	100.0	4944	13	US-10-001-189-56

ALIGNMENTS

RESULT 1

US-10-796-486-56

; Sequence 56, Application US/10796486

; Publication No. US20040171574A1

; GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/10/796.486

; CURRENT FILING DATE: 2004-03-08

; PRIOR APPLICATION NUMBER: US/09/628.730

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 56

; LENGTH: 3327

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH1-29Yalal522SK construct

US-10-796-486-56

Query Match	100.0%	Score 250;	DB 17;	Length 3327;
Best Local Similarity	100.0%;	Pred. No. 2.5e-73;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CACCTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGTGTGTACGGCAGCG	60	
Db	2575	CACCTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGTGTGTACGGCAGCG	2634	
Qy	61	TGACCGGTACACTTGTCCAGCGCCCTAGCGCCGCTTCCTTCCTTCCTTCCTTC	120	
Db	2635	TGACCGGTACACTTGTCCAGCGCCCTAGCGCCGCTTCCTTCCTTCCTTCCTTC	2694	

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 56.0345 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccctgacgcgcctgtacg.....ggttcacgtagtggccatc 250

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A-COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B-COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A-COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B-COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS-COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	250	100.0	3327	4	US-09-628-730-56
2	250	100.0	3369	4	US-09-628-730-48
3	250	100.0	3379	4	US-09-318-786-19
4	250	100.0	3450	4	US-09-318-786-20
5	250	100.0	3656	1	US-08-232-463-8
6	250	100.0	3688	1	US-08-232-463-9
7	250	100.0	3878	3	US-08-651-472-65
8	250	100.0	3878	3	US-08-358-928-65
9	250	100.0	3954	4	US-09-628-730-53
10	250	100.0	3954	4	US-09-628-730-57
11	250	100.0	3976	4	US-09-628-730-49
12	250	100.0	3988	4	US-09-358-856C-12
13	250	100.0	4435	2	US-08-792-824-1
14	250	100.0	4518	4	US-09-380-190A-26
15	250	100.0	4659	1	US-08-232-463-10
16	250	100.0	4665	3	US-08-948-378A-7
17	250	100.0	4665	3	US-09-169-425C-7
18	250	100.0	4665	4	US-09-759-960-7
19	250	100.0	4691	3	US-08-591-632-43
20	250	100.0	4691	3	US-09-611-451-43
21	250	100.0	4701	3	US-08-651-472-64
22	250	100.0	4701	3	US-08-358-928-64
23	250	100.0	4748	4	US-09-796-575-4
24	250	100.0	4818	1	US-08-232-463-11
25	250	100.0	4821	1	US-08-232-463-12
26	250	100.0	4824	1	US-08-232-463-13
27	250	100.0	4886	4	US-09-533-220A-4

```

c 28      250 100.0 4992 4 US-09-796-575-5 Sequence 5, Appli
c 29      250 100.0 4997 1 US-08-232-463-1 Sequence 1, Appli
c 30      250 100.0 5069 4 US-09-393-483A-1 Sequence 1, Appli
c 31      250 100.0 5069 4 US-09-393-483A-2 Sequence 2, Appli
c 32      250 100.0 5163 4 US-09-628-730-54 Sequence 54, Appli
c 33      250 100.0 5281 4 US-09-921-263-1 Sequence 1, Appli
c 34      250 100.0 5281 4 US-09-628-730-58 Sequence 58, Appli
c 35      250 100.0 5325 4 US-09-628-730-50 Sequence 50, Appli
c 36      250 100.0 5532 4 US-08-961-888-40 Sequence 40, Appli
c 37      250 100.0 5789 3 US-08-862-431-31 Sequence 32, Appli
c 38      250 100.0 5791 3 US-08-862-431-31 Sequence 31, Appli
c 39      250 100.0 5793 3 US-08-862-431-29 Sequence 29, Appli
c 40      250 100.0 5793 3 US-08-862-431-30 Sequence 30, Appli
c 41      250 100.0 5818 2 US-08-536-559A-3 Sequence 3, Appli
c 42      250 100.0 5819 2 US-08-536-559A-2 Sequence 2, Appli
c 43      250 100.0 5819 3 US-08-862-431-27 Sequence 27, Appli
c 44      250 100.0 5819 3 US-08-862-431-28 Sequence 28, Appli
c 45      250 100.0 5909 4 US-09-921-263-2 Sequence 2, Appli

```

ALIGNMENTS

RESULT 1

US-09-628-730-56

; Sequence 56, Application US/09628730

; Patent No. 6759393

; GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730

; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 56

; LENGTH: 3327

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH1-29Yala1522SK construct

US-09-628-730-56

Query Match Similarity 100.0%; Score 250; DB 4; Length 3327;

Best Local Similarity 100.0%; Pred. No. 1.le-64;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACCTGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTACGGCGAGCG 60

Db 2575 CACCTGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTACGGCGAGCG 2634

Qy 61 TGACCGCTACACTTGCCAGCGCCCTAGCGCGCGCTCTTCGCTTTCTCCCTTCCTTTC 120

Db 2635 TGACCGCTACACTTGCCAGCGCCCTAGCGCGCGCTCTTCGCTTTCTCCCTTCCTTTC 2694

Qy 121 TCGCCAGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTC 180

Db 2695 TCGCCAGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTC 2754

Qy 181 GATTAGTGTCTTACGGCACCTGACCCCAAAACCTGATTAGGGTGATGGTTCACGTA 240

Db 2755 GATTAGTGTCTTACGGCACCTGACCCCAAAACCTGATTAGGGTGATGGTTCACGTA 2814

Qy 241 GTGGGCCATC 250

Db 2815 GTGGGCCATC 2824

RESULT 2

US-09-628-730-48

; Sequence 48, Application US/09628730

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 264.607 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250
Perfect score: 250
Sequence: 1 caccctgagcgccctgtagc.....ggttcacgtagtgcccatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	250	100.0	2946	3	Aaa75650 Nucleotid
2	250	100.0	2958	2	Aaz11648 pBluescri
3	250	100.0	3327	4	Aac86263 Plasmid G
4	250	100.0	3327	6	Abk53274 Growth ho
5	250	100.0	3369	4	Aac86255 pGHRH-4
6	250	100.0	3369	6	Abk53266 Growth ho
7	250	100.0	3379	4	Aac66992 Vector pC
8	250	100.0	3417	6	Abq74934 Entry vec
9	250	100.0	3417	6	Abk90545 Vector DN
10	250	100.0	3417	6	Aad45825 EVE4 vect
11	250	100.0	3417	6	Abk90623 DNA seque
12	250	100.0	3417	10	Adc37163 Entry vec
13	250	100.0	3417	12	Adk01056 Entry vec
C 14	250	100.0	3450	4	Aac66993 Vector pC
C 15	250	100.0	3473	8	Abz57850 Plasmid p
C 16	250	100.0	3473	8	Abz80274 Peptide-1
17	250	100.0	3501	6	Abq74935 Entry vec
18	250	100.0	3501	6	Abk90546 Vector DN
19	250	100.0	3501	6	Adk45826 EVE5 vect
20	250	100.0	3501	6	Abk90624 DNA seque
21	250	100.0	3501	10	Adc37164 Entry vec

C 22	250	100.0	3501	12	ADK01057	Adk01057 Entry vec
C 23	250	100.0	3621	8	ABV77131	Abv77131 Nucleotid
C 24	250	100.0	3723	4	AD10000	Ad10000 Plasmid p
C 25	250	100.0	3747	2	ADH11242	Adh11242 Vertebrat
C 26	250	100.0	3851	12	ADP80954	Adp80954 Vector pD
C 27	250	100.0	3878	2	AAQ40299	Aaq40299 Sequence
C 28	250	100.0	3878	3	AAA89876	Aaa89876 Plasmid p
C 29	250	100.0	3878	4	AA12794	Aa12794 Plasmid p
C 30	250	100.0	3954	4	AAC86260	Aac86260 Plasmid G
C 31	250	100.0	3954	6	ABK53275	Abk53275 Growth ho
C 32	250	100.0	3954	6	ABK53271	Abk53271 Growth ho
C 33	250	100.0	3976	4	AAC86256	Aac86256 pGHRH1-44
C 34	250	100.0	3976	6	ABK53267	Abk53267 Growth ho
C 35	250	100.0	3988	2	AAx87639	Aax87639 Human por
C 36	250	100.0	3988	4	AAx72857	Aax72857 PDGB DNA
C 37	250	100.0	3988	10	ADB88985	Adb88985 Human por
C 38	250	100.0	3988	12	ADJ33442	Adj33442 Human por
C 39	250	100.0	4055	5	AA168460	Aa168460 Plasmid p
C 40	250	100.0	4151	12	ADK19677	Adk19677 Cloning v
C 41	250	100.0	4151	12	ADP03093	Adp03093 Enhanced
C 42	250	100.0	4163	3	AA29134	Aa29134 pNF-kappa
C 43	250	100.0	4188	6	ABQ74936	Abq74936 Entry vec
C 44	250	100.0	4188	6	ABK90547	Abk90547 Vector DN
C 45	250	100.0	4188	6	AAD45827	Aad45827 EVE8 vect

ALIGNMENTS

RESULT 1
AAA75650/c
ID AAA75650 standard; DNA; 2946 BP.
XX
AC AAA75650;
XX
DT 22-JAN-2001 (first entry)
XX
DE Nucleotide sequence of internal control plasmid pNW35.
XX
KW Genome genetic analysis; nucleic acid characterization; phenotype;
KW inter-population perfectly matched duplex depletion; plasmid pNW35; ss.
XX
OS Synthetic.
XX
PN WO200055364-A2.
XX
PD 21-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-GB000916.
XX
PR 12-MAR-1999; 99EP-00301933.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH UK LTD.
XX
PI Reeve MA, Workman NI, Martin-Parras L;
XX
DR WPI; 2000-602127/57.
XX
PT Genome analysis termed inter-population perfectly matched duplex
PT depletion, that overcomes limitations of current approach based on single
PT nucleotide polymorphism and linkage disequilibrium in isolated
XX
PS Example 1b; Page 121-122; 167pp; English.
XX
CC The specification describes method for whole genome genetic analysis. The
CC method is designated inter-population perfectly matched duplex depletion.
CC The method uses a mixture of DNA fragments enriched in fragments that are
CC characteristic of a phenotype of interest. The mixture of DNA fragments
CC is achieved by mixing fragments of affected and unaffected DNA under
CC hybridising conditions, and recovering a mixture of hybrids that contain
CC mismatches. The method is used for nucleic acid characterization. The
CC method can be also used to characterise several nucleic acid fragments of

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1214.56 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccgcgcgcgcctgtacg.....ggttcacgtagtggccatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	2858	12 CVPT218R	X70275 pUC18 and p
2	250	100.0	2946	6 BD237489	BD237489 Genetic a
3	250	100.0	2958	12 AF327874	AF327874 Cloning v
4	250	100.0	2958	12 AF327875	AF327875 Cloning v
5	250	100.0	2958	12 ARBLKSM	X52326 pBluescript
6	250	100.0	2958	12 ARBLKSM	X52324 pBluescript
7	250	100.0	3327	6 AX138937	AX138937 Sequence
8	250	100.0	3327	6 BD000702	BD000702 Growth ho
9	250	100.0	3369	6 AX138929	AX138929 Sequence
10	250	100.0	3369	6 BD000694	BD000694 Growth ho
11	250	100.0	3379	6 AR241677	AR241677 Sequence
12	250	100.0	3394	12 AF268280	AF268280 Phagemid
13	250	100.0	3417	6 CO779544	CO779544 Sequence
14	250	100.0	3417	6 AX492865	AX492865 Sequence
15	250	100.0	3417	6 AX494199	AX494199 Sequence
16	250	100.0	3417	6 AX496673	AX496673 Sequence
17	250	100.0	3417	6 AX592730	AX592730 Sequence
18	250	100.0	3417	6 AX811486	AX811486 Sequence
19	250	100.0	3450	6 AR241678	AR241678 Sequence

C 20	250	100.0	3451	12 AF268281	AF268281 Phagemid
C 21	250	100.0	3473	6 AX766168	AX766168 Sequence
C 22	250	100.0	3473	6 AX815026	AX815026 Sequence
C 23	250	100.0	3501	6 CO779545	CO779545 Sequence
C 24	250	100.0	3501	6 AX492866	AX492866 Sequence
C 25	250	100.0	3501	6 AX494200	AX494200 Sequence
C 26	250	100.0	3501	6 AX496674	AX496674 Sequence
C 27	250	100.0	3501	6 AX592731	AX592731 Sequence
C 28	250	100.0	3501	6 AX811487	AX811487 Sequence
C 29	250	100.0	3506	12 AF416744	AF416744 Cloning v
C 30	250	100.0	3602	12 AF327894	AF327894 Cloning v
C 31	250	100.0	3621	6 AX703433	AX703433 Sequence
C 32	250	100.0	3643	12 AF327895	AF327895 Expressio
C 33	250	100.0	3656	6 I66488	I66488 Sequence 8
C 34	250	100.0	3688	6 I66489	I66489 Sequence 9
C 35	250	100.0	3732	12 AF054625	AF054625 Reporter
C 36	250	100.0	3878	6 AX105796	AX105796 Sequence
C 37	250	100.0	3954	6 AX138934	AX138934 Sequence
C 38	250	100.0	3954	6 BD000699	BD000699 Growth ho
C 39	250	100.0	3976	6 AX138930	AX138930 Sequence
C 40	250	100.0	3976	6 BD000695	BD000695 Growth ho
C 41	250	100.0	3988	6 AR300373	AR300373 Sequence
C 42	250	100.0	3988	6 AX020190	AX020190 Sequence
C 43	250	100.0	3988	6 AX079036	AX079036 Sequence
C 44	250	100.0	3988	6 BD129691	BD129691 Therapeut
C 45	250	100.0	4027	12 RVU57024	RVU57024 Reporter ve

ALIGNMENTS

CVPT218R 2858 bp DNA linear SYN 07-OCT-1993
pUC18 and phage f1 derivative cloning vector.
X70275 1 GI:406850
ampicillin resistance; beta-galactosidase; phage f1; pUC18 plasmid.
synthetic construct
artificial sequences.

Mead,D.A., Szczesna-Skorupa,E. and Kemper,B.
Single-stranded DNA 'blue' T7 promoter plasmids: a versatile tandem
promoter system for cloning and protein engineering
Protein Eng. 1 (1), 67-74 (1986)
89184389
3507689

Pouwels,P.H., Enger-Valk,B.E. and Brammar,W.J.
This has no title
(in) Pouwels,P.H., Enger-Valk,B.E. and Brammar,W.J. (Eds.);
CLONING VECTORS, A LABORATORY MANUAL (SUPPL. UPDATE 1986): 1-1;
Elsevier, Amsterdam (1986)
3 (bases 1 to 2858)
Helmut,Bloecker.
Direct Submission
Submitted (07-JUL-1993) Helmut Bloecker F R G,
bloecker@venus.gbf-braunschweig.d400.de
See also Pharmacia catalogue 1993/4 for description details. also:
'New PTZ18R and PTZ19R multifunctional plasmids'; Analects
13:1-2(1985).

The sequence conflicts with the vecbase 3.x entry V80071, PTZ18R as
follows: G 251 should be deleted, C 822 should be deleted, G 1095
should be A, C 2557 is followed by an additional G, A 2563 should
be deleted, bases 2839 to 2849 should be deleted, T 2862 should be
C.
#parent VecBase(3):pUC18, VecSource(3):bcgal18,
VecSource(3):Prom77, GenBank(60):ficcg; #brother VecBase(3):pTZ19R.
Location/Qualifiers
1. .2858
/organism="synthetic construct"
/mol_type="other DNA"

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2303.51 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaagagtgtgtag.....cacatttcccgaaaagtgc 256

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hlc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190.2	74.3	971	9	CL121339	ISB1-80F2
2	185.4	72.4	266	2	AW494744	UI-M-BH3
3	185.4	72.4	453	6	CD284564	G39169.45
4	185.4	72.4	514	6	CB878095	HP07E24T
5	185.4	72.4	514	9	CL756923	OR_BBa012
6	185.4	72.4	516	9	CL587651	OB_Ba008
7	185.4	72.4	516	9	CL618531	OR_BBa001
8	185.4	72.4	516	9	CL618532	OR_BBa001
9	185.4	72.4	516	9	CL722827	OR_BBa005
10	185.4	72.4	516	9	CL744977	OR_BBa008
11	185.4	72.4	516	9	CL744978	OR_BBa008
12	185.4	72.4	516	9	CL756924	OR_BBa012
13	185.4	72.4	517	9	CL722626	OR_BBa005
14	185.4	72.4	609	9	AG048138	Pan trogl
15	185.4	72.4	616	9	AG124170	Pan trogl
16	185.4	72.4	618	9	AG114570	Pan trogl
17	185.4	72.4	619	9	AG054036	Pan trogl
18	185.4	72.4	620	9	AG064570	Pan trogl
19	185.4	72.4	621	9	AG071608	Pan trogl
20	185.4	72.4	621	9	AG108476	Pan trogl
21	185.4	72.4	626	9	AG133646	Pan trogl
22	185.4	72.4	627	9	AG083734	Pan trogl
23	185.4	72.4	627	9	AG097424	Pan trogl
24	185.4	72.4	637	9	AG051058	Pan trogl

C 25	185.4	72.4	638	9	AG065362	Pan trogl
C 26	185.4	72.4	639	9	AG082206	Pan trogl
C 27	185.4	72.4	640	9	AG093564	Pan trogl
C 28	185.4	72.4	642	9	AG044262	Pan trogl
C 29	185.4	72.4	643	9	AG065632	Pan trogl
C 30	185.4	72.4	644	9	AG094628	Pan trogl
C 31	185.4	72.4	644	9	AG140388	Pan trogl
C 32	185.4	72.4	646	9	AG084418	Pan trogl
C 33	185.4	72.4	647	9	AG043750	Pan trogl
C 34	185.4	72.4	648	6	CB878193	HP07K15T
C 35	185.4	72.4	648	9	AG090266	Pan trogl
C 36	185.4	72.4	654	9	AG045496	Pan trogl
C 37	185.4	72.4	656	9	AG095984	Pan trogl
C 38	185.4	72.4	659	9	AG041828	Pan trogl
C 39	185.4	72.4	659	9	AG053092	Pan trogl
C 40	185.4	72.4	659	9	AG062068	Pan trogl
C 41	185.4	72.4	659	9	AG068890	Pan trogl
C 42	185.4	72.4	659	9	AG073532	Pan trogl
C 43	185.4	72.4	660	9	AG058068	Pan trogl
C 44	185.4	72.4	661	9	AG047734	Pan trogl
C 45	185.4	72.4	661	9	AG068690	Pan trogl

ALIGNMENTS

RESULT 1
CL121339
LOCUS ISB1-80F23 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-80F23, 971 bp DNA linear GSS 05-JAN-2004
DEFINITION ISB1-80F23 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-80F23, genomic survey sequence.
ACCESSION CL121339
VERSION CL121339
KEYWORDS CL121339.1 GI:40614974
SOURCE GSS.
ORGANISM Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (Bases 1 to 971)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 15
High quality sequence stop: 604.
Location/Qualifiers
source
1. 971
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clones="ISB1-80F23"
/clone_lib="ISB1"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"

ORIGIN
Query Match 74.3%; Score 190.2; DB 9; Length 971;
Best Local Similarity 93.8%; Pred. No. 1.9e-45;
Matches 198; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1 TTCCGAAAAGAGTGTGTAGCTTTGATCGGCAAAACACCGCTGGTAGCGGTGGT 60
Db 91 TTCCGAAAAGAGTGTGTAGCTTTGATCGGCAAAACACCGCTGGTAGCGGTGGT 150
Qy 61 TTTTTCGTTTCGACGACGAGATTACCGCGCAGAAAAAGGATCTCAAGAGATCCCTTGT 120

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 57.3793 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955
Perfect score: 256
Sequence: 1 ttcgaaaaagagttgtag.....cacatttcccgaaagtgc 256

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	186.4	72.8	1360	3	US-09-082-649B-81
C 2	186	72.7	1360	3	US-09-082-649B-80
C 3	186	72.7	3987	3	US-09-082-649B-83
C 4	186	72.7	3987	3	US-09-082-649B-84
C 5	186	72.7	7612	4	US-09-700-934A-2
C 6	185.4	72.4	1905	1	US-08-594-469-9
C 7	185.4	72.4	1905	1	US-08-906-957-9
C 8	185.4	72.4	1947	3	US-09-025-769B-264
C 9	185.4	72.4	1947	4	US-09-490-070A-264
C 10	185.4	72.4	1947	4	US-09-490-153-264
C 11	185.4	72.4	2422	1	US-07-867-106-5
C 12	185.4	72.4	2462	4	US-09-496-445-5
C 13	185.4	72.4	2686	4	US-09-785-269C-11
C 14	185.4	72.4	2704	4	US-09-623-551-27
C 15	185.4	72.4	2755	2	US-07-916-098A-7
C 16	185.4	72.4	2839	4	US-09-809-517A-36
C 17	185.4	72.4	2865	4	US-09-795-872-9
C 18	185.4	72.4	2869	4	US-09-795-872-8
C 19	185.4	72.4	2927	2	US-08-941-647A-1
C 20	185.4	72.4	2927	3	US-09-142-481-14
C 21	185.4	72.4	2939	1	US-08-119-512-2
C 22	185.4	72.4	2939	1	US-08-488-015B-2
C 23	185.4	72.4	2939	3	US-08-814-412-17
C 24	185.4	72.4	2961	3	US-08-446-935-6
C 25	185.4	72.4	2973	4	US-09-402-266B-17
C 26	185.4	72.4	3003	6	5182260-18
C 27	185.4	72.4	3104	1	US-07-415-307A-1

28	185.4	72.4	3104	1	US-08-371-320-1	Sequence 1, Appli
29	185.4	72.4	3122	3	US-09-042-353-152	Sequence 152, App
30	185.4	72.4	3122	3	US-08-758-417A-416	Sequence 416, App
31	185.4	72.4	3130	3	US-09-038-141-1	Sequence 1, Appli
C 32	185.4	72.4	3138	1	US-07-867-106-4	Sequence 4, Appli
C 33	185.4	72.4	3175	4	US-09-646-075-2	Sequence 2, Appli
C 34	185.4	72.4	3190	4	US-09-027-169-6	Sequence 6, Appli
C 35	185.4	72.4	3249	1	US-08-507-455-4	Sequence 4, Appli
C 36	185.4	72.4	3266	2	US-08-737-316A-2	Sequence 2, Appli
C 37	185.4	72.4	3301	2	US-08-447-430A-42	Sequence 42, Appl
C 38	185.4	72.4	3301	4	US-09-342-673-42	Sequence 42, Appl
C 39	185.4	72.4	3307	3	US-09-401-171C-11	Sequence 11, Appl
C 40	185.4	72.4	3327	4	US-09-628-730-56	Sequence 56, Appl
C 41	185.4	72.4	3331	4	US-09-582-761B-32	Sequence 32, Appl
C 42	185.4	72.4	3343	6	5453363-2	Patent No. 5453363
C 43	185.4	72.4	3344	4	US-09-422-569-8	Sequence 8, Appli
C 44	185.4	72.4	3369	4	US-09-628-730-48	Sequence 48, Appl
C 45	185.4	72.4	3379	4	US-09-318-786-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-082-649B-81/c
; Sequence 81, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid DNA mutant Kanamycin resistance gene
US-09-082-649B-81

Query Match	72.8%	Score 186.4	DB 3	Length 1360
Best Local Similarity	99.5%	Pred. No. 4.1e-48		
Matches 187	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	TTCCGAAAAAGAGTTGGTAGCTTGTATCCGCGCAACCAACACCGCTGTAGCGGTGGT 60		
DB	1224	TTCCGAAAAAGAGTTGGTAGCTTGTATCCGCGCAACCAACACCGCTGTAGCGGTGGT 1165		
QY	61	TTTTTTTGTTCAGACGACGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTG 120		
DB	1184	TTTTTTTGTTCAGACGACGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTG 1105		
QY	121	ATCTTTTTCACGGGTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGGATTTTGGTC 180		
DB	1104	ATCTTTTTCACGGGTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGGATTTTGGTC 1045		
QY	181	ATGACCGG 188		
DB	1044	ATGACGCTG 1037		
RESULT 2				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 270.958 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaaagagtgttag.....cacatttccccgaaagtgc 256

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	4597	4	Aaf24901 Nucleotid
2	256	100.0	8115	6	Abag7958 Lactic ac
3	256	100.0	8115	6	Abag7959 Lactic ac
4	189.8	74.1	5195	6	Abq74554 Human Del
5	189.8	74.1	5195	12	Adm94827 Human dev
6	189.8	74.1	5566	6	Abn86160 Nucleotid
c 7	187.2	73.1	3851	12	Adp80954 Vector pD
c 8	187	73.0	1824	4	Aas41089 cDNA enco
c 9	187	73.0	1824	4	Aak57143 Human imm
10	186.8	73.0	6756	12	Adj57431 Vector pA
11	186.8	73.0	6757	6	Aas20498 Expressio
12	186.6	72.9	5875	6	Abz75111 VEGF expr
13	186.4	72.8	5742	6	Aas20504 Expressio
14	186.4	72.8	5742	12	Adj57437 Vector pY
15	186.4	72.8	10160	12	Adp84798 HIV subty
16	186.4	72.8	10186	12	Adp84796 Plasmid c
17	186.4	72.8	10198	12	Adp84799 HIV subty
18	186.2	72.7	5091	10	Adi39129 B. subtil
19	186.2	72.7	5091	12	Ado80519 Plasmid p
20	186.2	72.7	5091	12	Ado80585 Plasmid p
21	186.2	72.7	5091	12	Ado80330 Plasmid p

22	186.2	72.7	5156	10	Adf66614 RXN02910
23	186.2	72.7	5156	12	Adq31509 Vector pG
24	186.2	72.7	6087	10	Adf66615 Plasmid P
25	186.2	72.7	6087	12	Adq31510 RXN02910
26	186.2	72.7	8787	10	Adi39145 Plasmid p
c 27	186	72.7	1360	2	AAV74262 Plasmid p
c 28	186	72.7	1360	2	AAV83728 Plasmid p
c 29	186	72.7	3647	12	Adl90416 Clostridi
30	186	72.7	4204	3	Aac55522 Donor pla
31	186	72.7	4208	3	Aac55523 Donor pla
c 32	186	72.7	4470	3	Aac55521 Donor pla
c 33	186	72.7	4470	10	Abz58767 Destinati
c 34	186	72.7	4886	12	Adl90418 Clostridi
c 35	186	72.7	4892	9	Ada50329 Plasmid v
c 36	186	72.7	5076	12	Adl90417 Clostridi
37	186	72.7	5584	3	Aac55632 Donor pla
38	186	72.7	5584	10	Abz58766 Donor pla
39	186	72.7	7612	3	AAZ39629 DNA seque
40	185.6	72.5	9830	3	AAa96220 Nucleotid
41	185.6	72.5	10704	2	AAQ43846 Plasmid p
c 42	185.4	72.4	478	8	AAAD48705 Hygromyci
c 43	185.4	72.4	478	10	Adci3870 Oligonuci
c 44	185.4	72.4	695	2	AAV69310 E. coli o
c 45	185.4	72.4	941	12	Ado36316 Intracell

ALIGNMENTS

RESULT 1
AAF24901
ID AAF24901 standard; DNA; 4597 BP.
XX
AC AAF24901;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of the plasmid pCDNA3.1/GS.
XX

KW Microsphere; dihydrazide; hyaluronic acid; inflammatory response;
KW myocardial ischemia; cardiac angiogenesis; haemophilia;
KW vascular endothelial growth factor; VEGF; ss.
XX
OS Synthetic.
XX
FN WO200078358-A2.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US016837.
XX
PR 18-JUN-1999; 99US-0140260P.
XX

(COLL-) COLLABORATIVE GROUP LTD.
Chen W;
XX
DR WPI; 2001-071363/08.
XX

XX
PT Hyaluronic acid micro spheres for use in gene therapy of myocardial
PT ischemia and hemophilla, comprising dihydrazide derivatized hyaluronic
PT acids crosslinked to nucleic acids.
XX
XX Example 1; Page 36-38; 38pp; English.

XX
CC The specification describes a microsphere comprising dihydrazide
CC derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The
CC microspheres cause reduced inflammatory responses, and have increased
CC safety and biodegradability. The microspheres are useful for transfecting
CC a cell of a subject and for treating a subject having myocardial
CC ischemia, by increasing cardiac angiogenesis. They are also useful for
CC treating haemophilia. The present sequence represents the plasmid
CC pCDNA3.1/GS, into which is inserted a polynucleotide sequence which is

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1243.71 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955
Perfect score: 256
Sequence: 1 ttccgaaaaagattgtagt.....cacatttccccgaaaagtgc 256

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	3986	12	PCDNA3ZEO
2	256	100.0	4392	12	AF361441 Cloning vec
3	256	100.0	4597	6	AX060344 Cloning v
4	256	100.0	8115	6	AX060344 Sequence
5	256	100.0	8115	6	BD087749 Sequence
6	190	74.2	4419	12	BD087750 Shuttle v
7	189.8	74.1	5566	6	AY219688 Expressio
8	188.8	73.8	6023	12	AX451644 Sequence
9	187	73.0	4952	12	AF102577 Cloning v
10	187	73.0	131002	2	XXU14594 UI4594 Shuttle vec
11	186.8	73.0	6757	6	AC024392 Homo sapi
12	186.8	73.0	6757	6	CQ760746 Sequence
13	186.6	72.9	5874	6	AX451313 Sequence
14	186.6	72.9	5875	6	AX615156 Sequence
15	186.4	72.8	1360	6	AX754988 Sequence
16	186.4	72.8	4050	12	AR182909 Sequence
17	186.4	72.8	4227	12	AF053407 Expressio
18	186.4	72.8	4625	12	AF053408 Expressio
19	186.4	72.8	5742	6	AF053409 Expressio
					CQ760752 Sequence

20	186.4	72.8	5742	6	AX451319 Sequence
21	186.2	72.7	5091	6	CQ794458 Sequence
22	186.2	72.7	5091	6	CQ794562 Sequence
23	186.2	72.7	5091	6	CQ795592 Sequence
24	186.2	72.7	5091	6	AX930591 Sequence
25	186.2	72.7	5091	6	AX959595 Sequence
26	186.2	72.7	5156	6	CQ826646 Sequence
27	186.2	72.7	6087	6	CQ826647 Sequence
28	186.2	72.7	6142	6	CQ795604 Sequence
29	186.2	72.7	6472	6	CQ794470 Sequence
30	186.2	72.7	6591	6	CQ794576 Sequence
31	186.2	72.7	6631	6	AX959601 Sequence
32	186.2	72.7	6631	6	AX959605 Sequence
33	186.2	72.7	8384	12	AX265466 Shuttle v
34	186.2	72.7	8787	6	AX930607 Sequence
35	186	72.7	1360	6	AR182908 Sequence
36	186	72.7	2730	12	AY219701 Cloning v
37	186	72.7	3018	12	AF324725 Cloning v
38	186	72.7	3090	12	AF223640 Cloning v
39	186	72.7	3141	12	AF324726 Cloning v
40	186	72.7	3647	6	CQ794766 Sequence
41	186	72.7	3987	6	AR182910 Sequence
42	186	72.7	3987	6	AR182911 Sequence
43	186	72.7	4204	6	BD263378 Compositi
44	186	72.7	4208	6	BD263379 Compositi
45	186	72.7	4470	6	BD263377 Compositi

ALIGNMENTS

RESULT 1
PCDNA3ZEO 3986 bp DNA linear SYN 16-AUG-1995
Cloning vector pCDNA3ZEO DNA.
X90639.1 GI:949972
X90639.1 Cloning vector; expression vector; multiple cloning site; Plasmid.
KEYWORDS cloning vector; expression vector; multiple cloning site; Plasmid.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
Peters,H., Hundhausen,T., Kroenke,M. and Marget,M.
TITLE A new small sized high-level eukaryotic expression vector
JOURNAL Unpublished
AUTHORS Peters,H.
REFERENCE 2 (bases 1 to 3986)
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie,
Michaelisstr.5, D- 24105 Kiel, FRG
COMMENT Related sequences: M21295 and K03104.
FEATURES
source Location/Qualifiers
1..3986
/organism="synthetic construct"
/mol_type="other DNA"
/db_xref="taxon:32630"
/plasmid="pcDNA3ZEO"
1..2125
misc_feature /note="cloning vector (pcDNA3) (Invitrogen)"
889..994
misc_feature /note="multiple cloning site (MCS)"
2126..2796
misc_feature /note="Cloning vector (PzeoSV) (Invitrogen)"
2797..3986
misc_feature /note="cloning vector (pcDNA3)"

ORIGIN
Query Match 100.0%; Score 256; DB 12; Length 3986;
Best Local Similarity 100.0%; Pred. No. 8.4e-65;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAAAAAGATTGGTAGCTTTGATCCGCAACAAACACCGCTGGTAGCGTGGT 60
|||||

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1168.43 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaagagtggttag.....cacatttcccgaaaagtgc 256

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	4597	15	US-10-277-184-3
2	256	100.0	8115	9	US-09-778-516A-1
3	256	100.0	8115	9	US-09-778-516A-2
4	189.8	74.1	5195	16	US-10-419-045-2
5	189.8	74.1	5566	15	US-10-400-053-22
6	186.8	73.0	6757	9	US-09-896-594-16
7	186.8	73.0	6757	16	US-10-185-475-16
8	186.8	73.0	6757	16	US-10-185-475-16
9	186.4	72.8	1360	11	US-09-965-101-81
c	186.4	72.8	5742	9	US-09-896-594-22
10	186.4	72.8	5742	16	US-10-185-475-22
11	186.4	72.8	5742	16	US-10-185-475-22
12	186.4	72.8	5742	16	US-10-672-484-22

13	186.2	72.7	5156	15	US-10-307-138-12	Sequence 12, Appl
14	186.2	72.7	6087	15	US-10-307-138-13	Sequence 13, Appl
c	186	72.7	1360	11	US-09-965-101-80	Sequence 80, Appl
16	186	72.7	3647	15	US-10-241-596-134	Sequence 134, Appl
c	186	72.7	3715	17	US-10-446-629-5	Sequence 5, Appl
c	186	72.7	3741	17	US-10-446-629-4	Sequence 4, Appl
19	186	72.7	3987	11	US-09-965-101-83	Sequence 83, Appl
c	186	72.7	3987	11	US-09-965-101-84	Sequence 21, Appl
c	186	72.7	4470	15	US-10-151-690-21	Sequence 136, Appl
c	186	72.7	4886	15	US-10-241-596-136	Sequence 1, Appl
c	186	72.7	4892	15	US-10-357-268-1	Sequence 135, Appl
c	186	72.7	5076	15	US-10-241-596-135	Sequence 61, Appl
c	186	72.7	5584	15	US-10-151-690-61	Sequence 115, Appl
c	185.4	72.4	478	15	US-10-260-150-115	Sequence 267259,
c	185.4	72.4	641	13	US-10-027-632-267259	Sequence 267259,
c	185.4	72.4	641	15	US-10-027-632-267259	Sequence 1385, Ap
c	185.4	72.4	1150	9	US-09-764-868-1385	Sequence 1380, Ap
c	185.4	72.4	1796	9	US-09-764-868-1380	Sequence 8685, Ap
c	185.4	72.4	1796	10	US-09-764-891-8685	Sequence 6091, Ap
c	185.4	72.4	1953	9	US-09-974-300-6091	Sequence 5564, Ap
c	185.4	72.4	2210	10	US-09-764-891-5564	Sequence 5568, Ap
c	185.4	72.4	2212	10	US-09-764-891-5577	Sequence 5577, Ap
c	185.4	72.4	2212	10	US-09-764-891-5579	Sequence 5579, Ap
c	185.4	72.4	2212	10	US-09-764-891-5599	Sequence 5599, Ap
c	185.4	72.4	2212	10	US-09-764-891-5607	Sequence 5607, Ap
c	185.4	72.4	2212	10	US-09-764-891-5609	Sequence 5609, Ap
c	185.4	72.4	2213	10	US-09-764-891-5572	Sequence 5572, Ap
c	185.4	72.4	2213	10	US-09-764-891-5602	Sequence 5602, Ap
c	185.4	72.4	2297	10	US-09-891-865A-11	Sequence 11, Appl
c	185.4	72.4	2406	15	US-10-307-138-14	Sequence 14, Appl
c	185.4	72.4	2462	15	US-10-365-062-5	Sequence 5, Appl
c	185.4	72.4	2570	9	US-09-836-737A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-277-184-3
; Sequence 3, Application US/10277184
; Publication No. US20030114406A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Weiliam
; TITLE OF INVENTION: HYALURONIC ACID MICROSPHERES FOR
; FILE REFERENCE: 2055/1G717-US1
; CURRENT APPLICATION NUMBER: US/10/277,184
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/596,665
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 60/140,260
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCDNA3.1/GS vector by Invitrogen Corporation
US-10-277-184-3

Query Match	100.0%	Score 256;	DB 15;	Length 4597;
Best Local Similarity	100.0%	Pred. No. 6.6e-69;	Indels 0;	Gaps 0;
Matches 256;	Conservative 0;	Mismatches 0;		
Qy	1	TTCCGAAAAGAGTGGTGTAGCTTTGATCCGGCAAAACACCGCTGGTAGCGGTGGT 60		
Db	4331	TTCCGAAAAGAGTGGTGTAGCTTTGATCCGGCAAAACACCGCTGGTAGCGGTGGT 4390		
Qy	61	TTTTTTGTTTCAGACGACGATACGGCGGAGAAAAAGGATCTCAAGAGATCCTTTG 120		